

5' GGC TTC TGG GAG CNA CCG CTC CGC TCG TCT CGT TGG TTC CGG AGG TCG CTG CCG

CGG TGG GAA ATG CTG GCG CGC GCG GCG CGG GGG CAC TGG GGC CCT TTT GCT GAG

M L A R A A R G H W G P F A E

GGG CTC TCT ACT GGC TTC TGG CCG CGC TCC GGC CGC GCC TCC TCT GGA TTG CCC

G L S T G F W P R S G R A S S G L P

CGA AAC ACC GTG GTA CTG TTC GTG CCG CAG CAG GAG GCC TGG GTG GTG GAG CGA

R N T V V L F V P Q Q E A W V V E R

ATG GGC CGA TTC CAC CGG ATC CTG GAG CCT GGT TTG AAC ATC CTC ATC CCT GTG

M G R F H R I L E P G L N I L I P V

TTA GAC CGG ATC CGA TAT GTG CAG AGT CTC AAG GAA ATT GTC ATC AAC GTG CCT

L D R I R Y V Q S L K E I V I N V P

GAG CAG TCG GCT GTG ACT CTC GAC AAT GTA ACT CTG CAA ATC GAT GGA GTC CTT

E Q S A V T L D N V T L Q I D G V L

TAC CTG CGC ATC ATG GAC CCT TAC AAG GCA AGC TAC GGT GTG GAG GAC CCT GAG

Y L R I M D P Y K A S Y G V E D P E

TAT GCC GTC ACC CAG CTA GCT CAA ACA ACC ATG AGA TCA GAG CTC GGC AAA CTC

Y A V T Q L A Q T T M R S E L G K L

TCT NTG GAC AAA GTC TTC CGG GAA CGG GAG TCC CTG AAT GCC AGC ATT GTG GAT

S X D K V F R E R E S L N A S I V D

GCC ATC AAC CAA GCT GCT GAC TGC TGG GGT ATC CGC TGC CTN CGT TAT GAG ATC

A I N Q A A D C W G I R C L R Y E I

AAG GAT ATC CAT GTG CCA CCC CGG GTG AAA GAG TCT ATG CAG ATG CAG GTG GAG

K D I H V P P R V K E S M Q M Q V E

GCA GAG CGG CGG AAA CGG GCC ACA GTT CTA GAG TCT GAG GGG ACC CGA GAG TCG

A E R R K R A T V L E S E G T R E S

FIGURE 1A

711 720 729 738 747 756
 GCC ATC AAT GTG GCA GAA GGG AAG AAA CAG GCC CAG ATC CTG GCC TCC GAA GCA
 A I N V A E G K K Q A Q I L A S E A

765 774 783 792 801 810
 GAA AAG GCT GAA CAG ATA AAT CAG GCA GCA GGA GAG GCC AGT GCA GTT CTG GCG
 E K A E Q I N Q A A G E A S A V L A

819 828 837 846 855 864
 AAG GCC AAG GCT AAA GCT GAA GCT ATT CGA ATC CTG GCT GCA GCT CTG ACA CAA
 K A K A K A E A I R I L A A A L T Q

873 882 891 900 909 918
 CAT AAT GGA GAT GCA GCA GCT TCA CTG ACT GTG GCC GAG CAG TAT GTC AGC GCG
 H N G D A A A S L T V A E Q Y V S A

927 936 945 954 963 972
 TTC TCC AAA CTG GCC AAG GAC TCC AAC ACT ATC CTA CTG CCC TCC AAC CCT GGC
 F S K L A K D S N T I L L P S N P G

981 990 999 1008 1017 1026
 GAT GTC ACC AGC ATG GTG GCT CAG GCC ATG GGT GTA TAT GGA GCC CTC ACC AAA
 D V T S M V A Q A M G V Y G A L T K

1035 1044 1053 1062 1071 1080
 GCC CCA GTG CCA GGG ACT CCA GAC TCA CTC TCC AGT GGG AGC AGC AGA GAT GTC
 A P V P G T P D S L S S G S S R D V

1089 1098 1107 1116 1125 1134
 CAG GGT ACA GAT GCA AGT NTT GAT GAG GAA CTT GAT CGA GTC AAG ATG AGT TAG
 Q G T D A S X D E E L D R V K M S *

1143 1152 1161 1170 1179 1188
 TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT

3'

FIGURE 1B

FIGURE 2A

	789094
165 S -- D R E E I A H N M Q S T L D D A T D A W G I K V E R V E I K D I H V P P R	GI 31069
170 S -- D R E E T L A A S M Q T I L D E A T E S W G I K V E R V E I K D V R L P I Q	GI 1065452
197 SS Q D R R I I S A N L K D E L G S F T C Q F G V E I T D V E I S D V K I - -	GI 1353669
136 T -- S R D Q I N A Q L R G V L D D E A T G R W G L R V A R V E L R S I D P P P S	Z79701
134 N -- K R E Y I N S K L L E I L D R E T D A W G V R I E K V E V K E I D P P E D	GI 1591514
186 VKESMOMOVEAERRKRAATVLESEGTRESAINVAEGKKQAQ	789094
203 LQRAMAAEAESAERAKKVIAAEEEMNA - - - - -	GI 31069
208 LQRAMAAEAETREARAKVIAAEEGEQKA - - - - -	GI 1065452
234 VKEGENMGMSA - - - - - LS S VAKSDAGQQQLWQ	GI 1353669
174 IQASMEKQMKAADREKRAMIILTAEGTREAAIKQAEGQKQAQ	Z79701
172 IKNAMAQMKAEERLKRAAIIEAEEGKPE	GI 1591514
226 ILASEAEKAEQINOAAGEASAVALAKAKAKAEAII	789094
231 - - - - - SRALKEASMVI TE - - - - -	GI 31069
236 - - - - - SRALRDAASVIAQ - - - - -	GI 1065452
260 VIGP- - - - VFEDFAKECAAECKAKENA PLVDL - - - - -	GI 1353669
214 ILLAEGA[K]QAA[L]LA EA DRQSRLRAQGGERAAAYLQAQGGQ	Z79701
259 - RILAAAALTQHNGDAAAASLTVAEOYVSASFSLAKDSNTIL	789094
244 - - - - - SPAAQLRLRYLQTTLTITIAAEKNSTI	GI 31069
249 - - - - - SPAAQLRLRYLQTLSVAAREK - - - - -	GI 1065452
288 SDVPSTSAAGSTTDTPNIPSIDIDHLISVASLAMDEH - LV	GI 1353669
254 AKAI EKTFAAIKAGRPTPEMLLYQYLQTLPEMAARGDANKV	Z79701
298 - - - - - LPSPFGDVTSMVAAOAM - - GVYGALTKAPVGTPD	789094
268 - - - - - VFELPIDM - - - - -	GI 31069
269 - - - - - FDDHLPT - - - - -	GI 1065452
327 RLIGRVFOINCKDI EP - ICIDLKHGS[A]YKGTSL - NP[D]	GI 1353669
294 WVVP SDFNAALQGFT[R]LLGKPGE DGVF - RFEPSPVEDQP[K]	Z79701

FIGURE 2B

330	S L S S G S S R D V Q G	- - - - -	T D A S X D E E L D	- - - - -	R V K	- - - - -	789094
276	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	GI 31069
276	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	L GI 31069
364	V V F E - T S L E V F G	K I L T K E V S P V T V Y M N G N L K	V K	G S I Q D A M	GI 1353669		
333	H A A D G D D A E V A G W F S T D T D P S I A R A V A	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	GI 1353669
355	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	789094
277	Q - G I G A K H S H L G	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	GI 31069
277	D - G I - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	GI 1065452
403	Q L K H L V E R M S D W L	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	GI 1353669
370	E - G S L G T P P R L T Q	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	279701

2

Library	Lib Description	Abun	Pct	Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703	
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577	
TESTNOT03	testis, 37 M	1	0.0557	
LIVRNOT02	liver, 32 F	1	0.0515	
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418	
LVENNOT03	heart, left ventricle, 31 M	1	0.0336	
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309	
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288	
KERANOT01	keratinocytes, neonatal M	1	0.0227	
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194	
LUNGNOT04	lung, 2 M	1	0.0182	
PGANNT01	paraganglia, 46 M	1	0.0159	
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150	

FIGURE 3